RAW SEQUENCE LISTING   DATE: 11/28/2001
PATENT APPLICATION: US/09/841,805A   TIME: 11:32:06

Input Set : N:\Crf3\RULE60\09841805a.txt
Output Set: N:\CRF3\11282001\I841805A.raw

SEQUENCE LISTING

```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Lal, Preeti
 6                    Shah, Purvi
 7                    Corley, Neil C.
 9     (ii) TITLE OF INVENTION: HUMAN MEMBRANE RECYCLING
10                             PROTEINS
12    (iii) NUMBER OF SEQUENCES: 5
14     (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16          (B) STREET: 3174 Porter Dr.
17          (C) CITY: Palo Alto
18          (D) STATE: CA
19          (E) COUNTRY: USA
20          (F) ZIP: 94304
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Diskette
24          (B) COMPUTER: IBM Compatible
25          (C) OPERATING SYSTEM: DOS
26          (D) SOFTWARE: FastSEQ for Windows Version 2.0
28     (vi) CURRENT APPLICATION DATA:
29          (A) APPLICATION NUMBER: US/09/841,805A
30          (B) FILING DATE: 24-Apr-2001
31          (C) CLASSIFICATION:
33    (vii) PRIOR APPLICATION DATA:
34          (A) APPLICATION NUMBER: 09/360,125
35          (B) FILING DATE: 1999-07-23
37   (viii) ATTORNEY/AGENT INFORMATION:
38          (A) NAME: Billings, Lucy J.
39          (B) REGISTRATION NUMBER: 36,749
40          (C) REFERENCE/DOCKET NUMBER: PF-0456 US
42     (ix) TELECOMMUNICATION INFORMATION:
43          (A) TELEPHONE: 650-855-0555
44          (B) TELEFAX: 650-845-4166
47 (2) INFORMATION FOR SEQ ID NO: 1:
49      (i) SEQUENCE CHARACTERISTICS:
50          (A) LENGTH: 347 amino acids
51          (B) TYPE: amino acid
52          (C) STRANDEDNESS: single
53          (D) TOPOLOGY: linear
55    (vii) IMMEDIATE SOURCE:
56          (A) LIBRARY: TONGTUT01
57          (B) CLONE: 980615
59     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu
62  1               5                  10                  15
63 Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser
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C--> 29 (line 29)
C--> 30 (line 30)

ENTERED

Input Set : N:\Crf3\RULE60\09841805a.txt
Output Set: N:\CRF3\11282001\I841805A.raw

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64                    20                    25                    30
65  Arg Gln Tyr Ala Thr Leu Asp Val Tyr Asn Pro Phe Glu Thr Arg Glu
66            35                    40                    45
67  Pro Pro Pro Ala Tyr Glu Pro Pro Ala Pro Ala Pro Leu Pro Pro Pro
68            50                    55                    60
69  Ser Ala Pro Ser Leu Gln Pro Ser Arg Lys Leu Ser Pro Thr Glu Pro
70  65                    70                    75                    80
71  Lys Asn Tyr Gly Ser Tyr Ser Thr Gln Ala Ser Ala Ala Ala Ala Thr
72                      85                    90                    95
73  Ala Glu Leu Leu Lys Lys Gln Glu Glu Leu Asn Arg Lys Ala Glu Glu
74            100                   105                   110
75  Leu Asp Arg Arg Glu Arg Glu Leu Gln His Ala Ala Leu Gly Gly Thr
76            115                   120                   125
77  Ala Thr Arg Gln Asn Asn Trp Pro Pro Leu Pro Ser Phe Cys Pro Val
78            130                   135                   140
79  Gln Pro Cys Phe Phe Gln Asp Ile Ser Met Glu Ile Pro Gln Glu Phe
80  145                   150                   155                   160
81  Gln Lys Thr Val Ser Thr Met Tyr Tyr Leu Trp Met Cys Ser Thr Leu
82                      165                   170                   175
83  Ala Leu Leu Leu Asn Phe Leu Ala Cys Leu Ala Ser Phe Cys Val Glu
84            180                   185                   190
85  Thr Asn Asn Gly Ala Gly Phe Gly Leu Ser Ile Leu Trp Val Leu Leu
86            195                   200                   205
87  Phe Thr Pro Cys Ser Phe Val Cys Trp Tyr Arg Pro Met Tyr Lys Ala
88            210                   215                   220
89  Phe Arg Ser Asp Ser Ser Phe Asn Phe Phe Val Phe Phe Phe Ile Phe
90  225                   230                   235                   240
91  Phe Val Gln Asp Val Leu Phe Val Leu Gln Ala Ile Gly Ile Pro Gly
92            245                   250                   255
93  Trp Gly Phe Ser Gly Trp Ile Ser Ala Leu Val Val Pro Lys Gly Asn
94            260                   265                   270
95  Thr Ala Val Ser Val Leu Met Leu Leu Val Ala Leu Leu Phe Thr Gly
96            275                   280                   285
97  Ile Ala Val Leu Gly Ile Val Met Leu Lys Arg Ile His Ser Leu Tyr
98            290                   295                   300
99  Arg Arg Thr Gly Ala Ser Phe Gln Lys Ala Gln Gln Glu Phe Ala Ala
100 305                   310                   315                   320
101 Gly Val Phe Ser Asn Pro Ala Val Arg Thr Ala Ala Ala Asn Ala Ala
102            325                   330                   335
103 Ala Gly Ala Ala Glu Asn Ala Phe Arg Ala Pro
104            340                   345
106 (2) INFORMATION FOR SEQ ID NO: 2:
108       (i) SEQUENCE CHARACTERISTICS:
109             (A) LENGTH: 1521 base pairs
110             (B) TYPE: nucleic acid
111             (C) STRANDEDNESS: single
112             (D) TOPOLOGY: linear
114       (vii) IMMEDIATE SOURCE:
115             (A) LIBRARY: TONGTUT01
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RAW SEQUENCE LISTING   DATE: 11/28/2001
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Input Set : N:\Crf3\RULE60\09841805a.txt
Output Set: N:\CRF3\11282001\I841805A.raw

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116          (B) CLONE: 980615
118    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120    NGACGCAGGC GCAACCCACG GCTGCTGCGG GGATCCTTGT GGCCCTTCCG GTCGATGGAA      60
121    CCAATCCGTG CACAGAGAAG CGGGGCGAAC TGAGGCGAGT GAAGTGGACT CTGAGGGCTA     120
122    CCGCTACCGC CACTGCTGCG GCAGGGGCGT GGAGGGCAGA GGGCCGCGGA GGCCGCAGTT     180
123    GCAAACATGG CTCAGAGCAG AGACGGCGGA AACCCGTTCG CCGAGCCCAG CGAGCTTGAC     240
124    AACCCCTTTC AGGACCCAGC TGTGATCCAG CACCGACCCA GCCGGCAGTA TGCCACGCTT     300
125    GACGTCTACA ACCCTTTTGA GACCCGGGAG CCACCACCAG CCTATGAGCC TCCAGCCCCT     360
126    GCCCCATTGC CTCCACCCTC AGCTCCCTCC TTGCAGCCCT CGAGAAAGCT CAGCCCCACA     420
127    GAACCTAAGA ACTATGGCTC ATACAGCACT CAGGCCTCAG CTGCAGCAGC CACAGCTGAG     480
128    CTGCTGAAGA AACAGGAGGA GCTCAACCGG AAGGCAGAGG AGTTGGACCG AAGGGAGCGA     540
129    GAGCTGCAGC ATGCTGCCCT GGGGGGCACA GCTACTCGAC AGAACAATTG GCCCCCTCTA     600
130    CCTTCTTTTT GTCCAGTTCA GCCCTGCTTT TTCCAGGACA TCTCCATGGA GATCCCCCAA     660
131    GAATTTCAGA AGACTGTATC CACCATGTAC TACCTCTGGA TGTGCAGCAC GCTGGCTCTT     720
132    CTCCTGAACT TCCTCGCCTG CCTGGCCAGC TTCTGTGTGG AAACCAACAA TGGCGCAGGC     780
133    TTTGGGCTTT CTATCCTCTG GGTCCTCCTT TTCACTCCCT GCTCCTTTGT CTGCTGGTAC     840
134    CGCCCCATGT ATAAGGCTTT CCGGAGTGAC AGTTCATTCA ATTTCTTCGT TTTCTTCTTC     900
135    ATTTTCTTCG TCCAGGATGT GCTCTTTGTC CTCCAGGCCA TTGGTATCCC AGGTTGGGGA     960
136    TTCAGTGGCT GGATCTCTGC TCTGGTGGTG CCGAAGGGCA ACACAGCAGT ATCCGTGCTC    1020
137    ATGCTGCTGG TCGCCCTGCT CTTCACTGGC ATTGCTGTGC TAGGAATTGT CATGCTGAAA    1080
138    CGGATCCACT CCTTATACCG CCGCACAGGT GCCAGCTTTC AGAAGGCCCA GCAAGAATTT    1140
139    GCTGCTGGTG TCTTCTCCAA CCCTGCGGTG CGAACCGCAG CTGCCAATGC AGCCGCTGGG    1200
140    GCTGCTGAAA ATGCCTTCCG GGCCCCGTGA CCCCTGACTG GGATGCCCTG GCCCTGCTAC    1260
141    TTGAGGGAGC TGACTTAGCT CCCGTCCCTA AGGTCTCTGG GACTTGGAGA GACATCACTA    1320
142    ACTGATGGCT CCTCCGTAGT GCTCCCAATC CTATGGCCAT GACTGCTGAA CCTGACAGGC    1380
143    GTGTGGGGAG TTCACTGTGA CCTAGTCCCC CCATCAGGCC ACACTGCTGC CACCTCTCAC    1440
144    ACGCCCCAAC CCAGCTTCCC TCTGCTGTGC CACGGCTGTT GCTTCGGTTA TTTAAATAAA    1500
145    AAGAAAGTGG AACTGGAACT G                                            1521
147 (2) INFORMATION FOR SEQ ID NO: 3:
149       (i) SEQUENCE CHARACTERISTICS:
150           (A) LENGTH: 329 amino acids
151           (B) TYPE: amino acid
152           (C) STRANDEDNESS: single
153           (D) TOPOLOGY: linear
155     (vii) IMMEDIATE SOURCE:
156           (A) LIBRARY: BRSTNOT01
157           (B) CLONE: 412453
159      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
161    Met Ser Ala Phe Asp Thr Asn Pro Phe Ala Asp Pro Val Asp Val Asn
162    1               5                   10                  15
163    Pro Phe Gln Asp Pro Ser Val Thr Gln Leu Thr Asn Ala Pro Gln Gly
164            20                  25                  30
165    Gly Leu Ala Glu Phe Asn Pro Phe Ser Glu Thr Asn Ala Ala Thr Thr
166            35                  40                  45
167    Val Pro Val Thr Gln Leu Pro Gly Ser Ser Gln Pro Ala Val Leu Gln
168        50                  55                  60
169    Pro Ser Val Glu Pro Thr Gln Pro Thr Pro Gln Ala Val Val Ser Ala
170    65                  70                  75                  80
171    Ala Gln Ala Gly Leu Leu Arg Gln Gln Glu Glu Leu Asp Arg Lys Ala
```

```
172                 85              90                95
173  Ala Glu Leu Glu Arg Lys Glu Arg Glu Leu Gln Asn Thr Val Ala Asn
174          100                 105               110
175  Leu His Val Arg Gln Asn Asn Trp Pro Pro Leu Pro Ser Trp Cys Pro
176          115                 120               125
177  Val Lys Pro Cys Phe Tyr Gln Asp Phe Ser Thr Glu Ile Pro Ala Asp
178      130               135               140
179  Tyr Gln Arg Ile Cys Lys Met Leu Tyr Tyr Leu Trp Met Leu His Ser
180  145               150               155               160
181  Val Thr Leu Phe Leu Asn Leu Leu Ala Cys Leu Ala Trp Phe Ser Gly
182          165                 170               175
183  Asn Ser Ser Lys Gly Val Asp Phe Gly Leu Ser Ile Leu Trp Phe Leu
184          180                 185               190
185  Ile Phe Thr Pro Cys Ala Phe Leu Cys Trp Tyr Arg Pro Ile Tyr Lys
186          195                 200               205
187  Ala Phe Arg Ser Asp Asn Ser Phe Ser Phe Phe Val Phe Phe Phe Val
188      210               215               220
189  Phe Phe Cys Gln Ile Gly Ile Tyr Ile Ile Gln Leu Val Gly Ile Pro
190  225               230               235               240
191  Gly Leu Gly Asp Ser Gly Trp Ile Ala Ala Leu Ser Thr Leu Asp Asn
192          245                 250               255
193  His Ser Leu Ala Ile Ser Val Ile Met Met Val Val Ala Gly Phe Phe
194          260                 265               270
195  Thr Leu Cys Ala Val Leu Ser Val Phe Leu Leu Gln Arg Val His Ser
196          275                 280               285
197  Leu Tyr Arg Arg Thr Gly Ala Ser Phe Gln Gln Ala Gln Glu Glu Phe
198      290                 295               300
199  Ser Gln Gly Ile Phe Ser Ser Arg Thr Phe His Arg Ala Ala Ser Ser
200  305               310               315               320
201  Ala Ala Gln Gly Ala Phe Gln Gly Asn
202                  325
```

204 (2) INFORMATION FOR SEQ ID NO: 4:
206   (i) SEQUENCE CHARACTERISTICS:
207   (A) LENGTH: 2434 base pairs
208   (B) TYPE: nucleic acid
209   (C) STRANDEDNESS: single
210   (D) TOPOLOGY: linear
212   (vii) IMMEDIATE SOURCE:
213   (A) LIBRARY: BRSTNOT01
214   (B) CLONE: 412453
216   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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218  NCCGGAAGTG GAGGGTCTAC ACGAAGCGCC GCTGGGTCTG GGTGCCCGGA GGCAGCAGCG   60
219  TTCGCGGAGT TCGCCCGCTG GCCCCCGATC ACCATGTCGG CTTTCGACAC CAACCCCTTC  120
220  GCGGACCCAG TGGATGTAAA CCCCTTCCAG GATCCCTCTG TGACCCAGCT GACCAACGCC  180
221  CCGCAGGGCG GCCTGGCGGA ATTCAACCCC TTCTCAGAGA CAAATGCAGC GACAACAGTT  240
222  CCTGTCACCC AACTCCCTGG GTCCTCACAG CCAGCGGTTC TCCAGCCATC AGTGGAACCA  300
223  ACCCAGCCGA CCCCCCAGGC CGTGGTGTCT GCAGCCCAGG CAGGCCTGCT CCGGCAGCAG  360
224  GAAGAACTGG ACAGGAAAGC TGCCGAGCTG AACGCAAGG AGCGGGAGCT GCAGAACACT  420
225  GTAGCCAACT TGCATGTGAG ACAGAACAAC TGGCCCCCTC TGCCCTCGTG GTGCCCTGTG  480
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226  AAGCCCTGCT TCTATCAGGA TTTCTCCACA GAGATCCCTG CCGACTACCA GCGGATATGC   540
227  AAGATGCTCT ACTATCTGTG GATGTTGCAT TCAGTGACTC TGTTTCTGAA CCTGCTTGCC   600
228  TGCCTGGCCT GGTTCTCGGG CAACAGCTCC AAGGGAGTGG ACTTTGGCCT CTCCATCCTG   660
229  TGGTTTCTGA TCTTCACTCC CTGTGCCTTC CTTTGTTGGT ACCGACCCAT CTATAAGGCC   720
230  TTTAGGTCCG ACAACTCTTT CAGCTTCTTT GTGTTCTTCT TTGTATTTTT TTGTCAAATA   780
231  GGGATCTACA TCATCCAGTT GGTTGGCATC CCTGGCCTGG GGACAGCGG TTGGATTGCA    840
232  GCCCTGTCTA CACTGGATAA TCATTCCCTG GCCATATCAG TCATCATGAT GGTGGTGGCT   900
233  GGCTTCTTCA CCCTCTGTGC CGTGCTCTCA GTCTTCCTCC TGCAGCGGGT GCACTCCCTC   960
234  TACCGACGGA CAGGGGCCAG CTTCCAGCAG GCCCAGGAGG AGTTTTCCCA GGGCATCTTC   1020
235  AGCAGCAGAA CCTTCCACAG AGCTGCTTCA TCTGCTGCCC AAGGAGCCTT CCAGGGGAAT   1080
236  TAGTCCTCCT CTCTTCTCTC CCCCTCAGCC TTTCTCTCGC CTGCCTTCTG AGCTGCACTT   1140
237  TCCGTGGGTG CCTTATGTGG TGGTGGTTGT GCCCAGCACA GACCTGGCAG GGTTCTTGCC   1200
238  GTGGCTCTTC CTCCTCCCTC AGCGACCAGC TCTCCCTGGA ACGGGAGGGA CAGGGAATTT   1260
239  TTTCCCCCTC TATGTACAAA AAAAAACAAA GCTCTCTTTC CTTCTCTGGT GATGGTTTGG   1320
240  TAGGATTCTT TTGTCTCTGG AAGCAGTGGG ACTGAAGTTC TCTTCGTCCT GTGCACACAC   1380
241  AGACACCCCC ACACAGTTGG GATCACAGGC TGACCTGGGC CCATCCCAGC TGGAGCTTTC   1440
242  TGCCAGGGTC CTGGGCCTTG ACTCCCCCAC CCTGCAGGCC TGGCCTGAAT CTGGCTTCTT   1500
243  AGACACAGCC CAGTCCTTCC TGCCTGGGCT GGGAATAAGC CTCTCACAGG TTCTGGTGGA   1560
244  CAGATCTGTT CCCCAGGTCA CTCCAGTGGT CTCCAGGCTT CCAGAGAAGG CTGGTTGCCT   1620
245  CAAGCTCTTC TCTGCCTCAT AAACGGATCC AGAGAAGGCT GGTTGCCTTA AGCTCTTCCC   1680
246  TGCCTCGTGT TCCTGAGAAA CGGATTAATA GCCCTTTATC CCCCTGCACC CTCCTGCAGG   1740
247  GGATGGCACT TTGAGCCCTC TGGAGCCCTC CCCTTGCTGA GCCTTACTCT CTTCAGACTT   1800
248  TCTGAATGTA CAGTGCCGTT GGTTGGGATT TGGGGACTGG AAGGGACCAA GGACACTGAC   1860
249  CCCAAGCTGT CCTGCCTAGC GTCCAGCGTC TTCTAGGAGG GTGGGGTCTG CCTGTCCTGG   1920
250  TGTGGTTGGT TTGGCCCTGT TTGCTGTGAC TACCCCCCCC CCTCCCCGAA CCGAGGGACG   1980
251  GCTGCCTTTG TCTCTGCCTC AGATGCCACC TGCCCCGCCC ATGCTCCCCA TCAGCAGCAT   2040
252  CCAGACTTTC AGGAAGGGCA GGACCAGCCA GTCCAGAACC GCATCCCTCA GCAGGGACTG   2100
253  ATAAGCCATC TCTCGGAGGG CCCCCTAATA CCCAGTGGAG TCTGGTTCAC ACCCTGGGGG   2160
254  GTGTGTCACT GTGATGGGAC ACGTAGGAGT CCACCCTTAA AACCAGCACC CTGTCCCTCG   2220
255  AGGCTGCCGA GTGGGTGTGT GGACTGGGGT GCCTTCCCAC AAAACTAGCC TCCGGCTCTG   2280
256  GGCCCGAGAC AGCCGCAGGC CCCAGCCACT GAATGATACT GGCAGCGGCT GGGGTTTTAT   2340
257  GAACTCCTTT CTGGTATTTT TTCCCCTCTA TGTACAAATG TATATGTTAC GTCTCAATTT   2400
258  TTGTGCTTAA GTAAAAATAA AAACATTTTC AGAC                               2434
```

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260  (2) INFORMATION FOR SEQ ID NO: 5:
262       (i) SEQUENCE CHARACTERISTICS:
263            (A) LENGTH: 338 amino acids
264            (B) TYPE: amino acid
265            (C) STRANDEDNESS: single
266            (D) TOPOLOGY: linear
268      (vii) IMMEDIATE SOURCE:
269            (A) LIBRARY: GenBank
270            (B) CLONE: 487057
272      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
274  Met Ser Asp Phe Asp Ser Asn Pro Phe Ala Asp Pro Asp Leu Asn Asn
275  1               5                   10                  15
276  Pro Phe Lys Asp Pro Ser Val Thr Gln Val Thr Arg Asn Val Pro Pro
277              20                  25                  30
278  Gly Leu Asp Glu Tyr Asn Pro Phe Ser Asp Ser Arg Thr Pro Pro Pro
279          35                  40                  45
```

VERIFICATION SUMMARY   DATE: 11/28/2001
PATENT APPLICATION: US/09/841,805A   TIME: 11:32:07

Input Set : **N:\Crf3\RULE60\09841805a.txt**
Output Set: **N:\CRF3\11282001\I841805A.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]